Genetic Parameters for Number of Piglets Born Alive Using a Random Regression Model

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SUMMARY

A random regression model (RRM) was applied to estimate dispersion parameters for number of piglets born alive (NBA) from first to tenth parity. Random regressions on Legendre polynomials of standardized parity were included for common litter environmental, permanent environmental and additive genetic effects. Estimated phenotypic variance and variance components (ratios) for NBA changed over parities and differed between farms. Eigenvalues for additive genetic effect were calculated in order to detect the proportion of additive genetic variability explained with individual production curves of animals. Existence of the 10-20 % genetic variability in the shape of the curves confirms a possibility for selection on persistency in litter size.

KEY WORDS

random regression, genetic parameters, litter size, pigs

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INTRODUCTION

In animal breeding, both repeatability and multiple-trait models have been applied to analyze traits that are measured more than once in lifetime of an animal. A repeatability model assumes genetic correlations of one between subsequent observations and a constant variance along trajectory. Multiple-trait analyses supposes subsequent observations to be different traits. More appropriate way of dealing with such traits is to fit a set of random regression coefficients describing production over time for each animal (Meyer, 1998). Main advantages of the random regression models (RRMs) in comparison to multiple-trait models are: requirement of fewer parameters to describe longitudinal data, smoother and with less bias (co)variance estimates, as well as possibility to predict covariance structure and breeding value of animal at any point along trajectory. In pigs, RRMs were mainly used for growth and feed intake. In the last decade, litter size has become a major component of selection goals in maternal lines and in some populations significant annual genetic trends have been obtained (Rothchild and Bidanel, 1998). Although litter size differs from fattening traits, some authors suggest that RRMs could be applied in selection on this trait. Possible genetic differences in litter size along the trajectory could be identified with RRMs and persistency in litter size could be used to select breeding sows (Huisman, 2002).

The aim of this paper was to estimate genetic and environmental dispersion parameters using RRM with Legendre (LG) polynomials of different power for number of piglets born alive (NBA) and compare results between three farms.

MATERIAL AND METHODS

Litter records data from three large Slovenian pig farms (A, B, C) from first to tenth parity, collected between January 1990 and December 2002, were analyzed separately. Individual litter records were excluded from analyses if traits were outside a given range. Previous lactation length and weaning to conception interval for sows had to be within 1-60 and 1-80 days, respectively. After data editing, 118079, 99411 and 70034 litter records were analysed for farm A, B and C, respectively (Table 1). Farms B and C had similar data structure regarding the number of litters per female (farm B = 3.56, farm C = 3.65) and smaller in comparison to farm A (4.16). All farms had similar number of animals that shared the same litter environment (farm A = 1.46, farm B = 1.49 and farm C = 1.40). There were some differences in number of progenies per sire (farm A = 30.79, farm B = 45.01 and farm C = 25.59).

For estimation of dispersion parameters for NBA the following RRM presented in scalar notation, was used:

$$y_{ijklmno} = \mu + B_i + S_j + P_k + W_l + \\ + b_{I\,k}\left(x_{ijklmno} - \bar{x}\right) + b_{II\,k}\left(x_{ijklmno} - \bar{x}\right)^2 + b_{III}\left(z_{ijklmno} - \bar{z}\right) + \\ + \sum_{}^{3}\sum_{}^{k}\alpha_{sm}\Phi_m\left(p^*_{ijklmno}\right) + \varepsilon_{ijklmno}$$

where $y_{ijklmno}$ is NBA, B_i, S_j, P_k and W_l are fixed effects of genotype, mating season (year-month interaction), parity and weaning to conception interval, respectively. Weaning to conception interval was defined as effect with classes (1-3, 4, 5, 6, 7, 8, 9, 10-23, 24-33 and 34-70 days). Age at farrowing ($x_{ijklmno}$) was modelled as quadratic regression nested within parity. Previous lactation length ($z_{ijklmno}$) was fitted as linear regression. Statistical package SAS (SAS Institute, 2001) was used for development of fixed part of the model.

Random regressions on orthogonal LG polynomials of standardized parity (p^*) were included for direct additive genetic, permanent environmental and common litter environmental effect. A standardized parity (p^*), with range from -1 to +1, was derived as

$$p^* = \frac{2*\left(p - p_{\min}\right)}{\left(p_{\max} - p_{\min}\right)} - 1,$$

where p_{min} is the first parity and p_{max} is the last parity (tenth) in the data.

Legendre polynomials from the linear power (LG1) with two terms to cubic power (LG3) with four terms were fitted. Estimation of (co)variance components

Table 1. Data and pedigree structure

	Farm A	Farm B	Farm C
No. of litter records	118079	99411	70034
No. of breeding females	28364	27912	19170
Litters per female	4.16	3.56	3.65
Females per common litter	1.46	1.49	1.40
Progenies per sire	30.79	45.01	25.59
Progenies per dam	2.79	3.14	2.47
No. of animals with records	28364	27912	19170
No. of ancestors	10734	4823	4367
No. of base animals	3973	1224	872

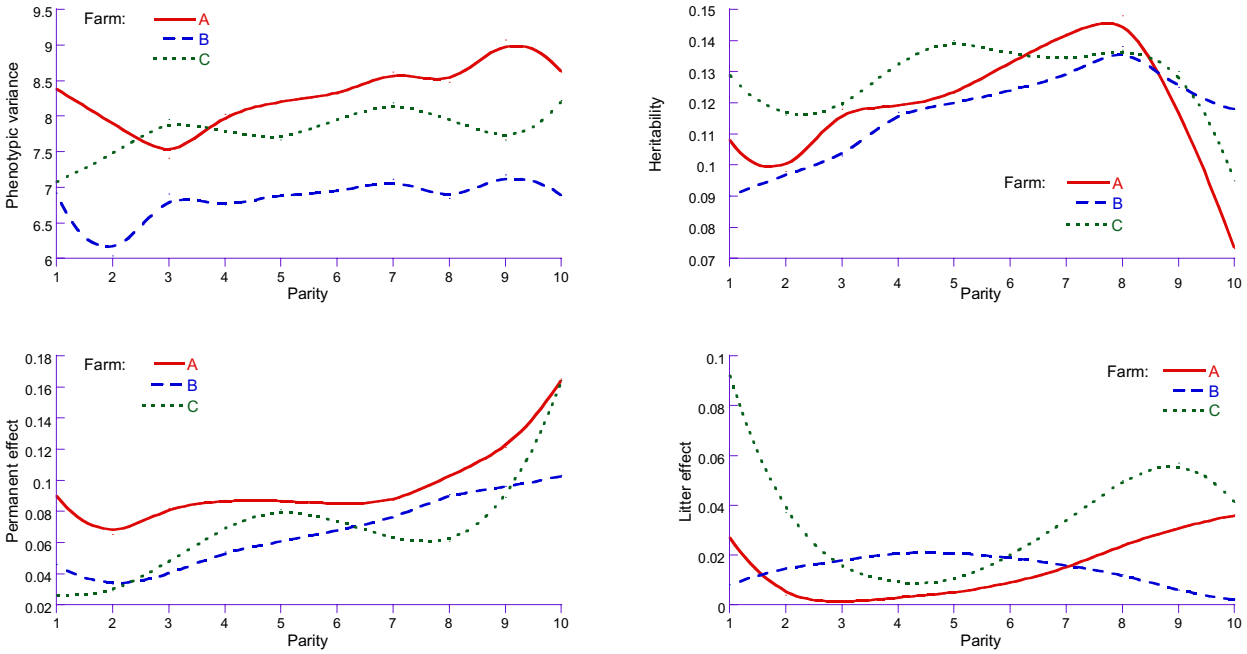

Figure 1. Phenotypic variances and proportions of the phenotypic variance over parities with Legendre polynomials of the cubic power for number of piglets born alive

from RRM was based on Residual Maximum Likelihood (REML) method using the VCE-5 software package (Kovač and Groeneveld, 2002). Additionally, modul SAS/IML (SAS Institute, 2001) was used for computation of eigenvalues for covariance matrices of regression coefficients to quantify contribution of higher orders of LG polynomials. Dispersion parameters estimated by REML were used to obtain solutions for fixed and random effects in model. Predicted random regression coefficients for additive genetic effect were used for calculation of breeding value for NBA along trajectory.

RESULTS AND DISCUSSION

The estimated phenotypic variances and ratios were presented in Figure 1. The estimates of phenotypic variance showed small increase from first to tenth parity. Also, phenotypic variances for farm B differed in comparison to other two farms. Heritabilities for all three farms ranged from 0.09 to 0.14. At the end of trajectory decrease in heritability was noticed, probably as a consequence of selection in previous parities and small number of data in the last parities. Permanent environmental effect (expressed as a ratio) generally increased over parities and ranged from 0.02 for farm C in first parity to 0.16 for farm A in tenth parity. Magnitudes of common litter environmental effect (expressed as ratio) were generally small, ranged from 0.01 to 0.02. There were some differences in shape of curves between farms.

Eigenvalues for Legendre polynomials from linear to cubic power for all three farms were computed (Table2). The eigenvalues of genetic covariance functions showed that the constant (zero) term accounted between 80 and 90 % of the additive genetic variability for NBA. This means that 10 to 20 % of variability was explained by individual genetic curves of sows. This proportion of variability was mainly covered by linear (8.2 to 15.7 %) and quadratic (2.5 to 4.4 %) coefficients. These values are higher compared to our previous study only for farm A that included litter records from first to sixth parity (Luković et al., 2003). Also, the eigenvalues of covariance functions showed a quadratic Legendre polynomial with three regression coefficients to be sufficient to explain all additive genetic variability. Although, this study considered equal power of Legendre polynomials in order to provide equal opportunity of variation for all random effects,

Table 2. Eigenvalues (%) for additive genetic effect with different power of LG polynomials

	Farm A			Farm B			Farm C		
Eigenvalues	LG1	LG2	LG3	LG1	LG2	LG3	LG1	LG2	LG3
0th	90.4	86.9	86.1	91.2	88.7	87.5	84.3	83.0	80.1
1st	9.6	10.1	11.0	8.8	8.2	8.6	15.7	14.5	14.9
2nd		3.0	2.9		3.1	3.2		2.5	4.4
3rd			0.0			0.7			0.0

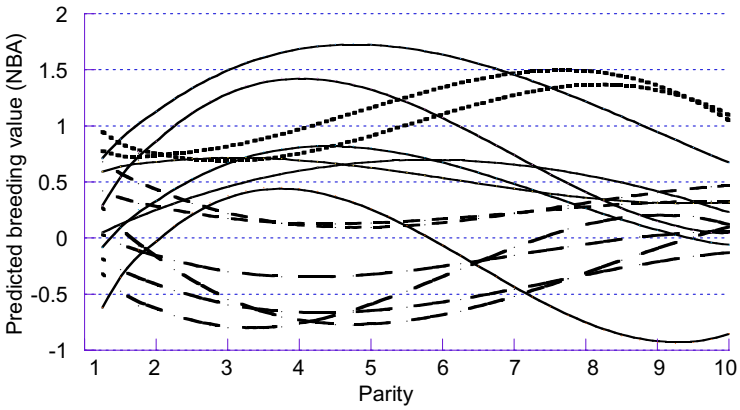

Figure 2.
Predicted breeding values for number of piglets born alive over parities for fourteen boars

some evidence has been found in favor to a lower order needed for the genetic than for the permanent environmental effect (Van der Werf et al., 1998).

The solutions from RRM with cubic power for the random regression coefficients of animals were used to compute breeding values for NBA along trajectory. The curves for fourteen boars with number of progenies between 500 and 850 showed that genetic merit function vary between individual animals (Figure 2). Choosing boars whose predicted breeding value increases over parities seems possible to change shape of curves for NBA of sows.

CONCLUSION

Parameters of dispersion for number of pigs born alive changed over parities and differed between populations. The existence of 10 to 20 % of non-constant additive genetic variation for NBA indicates that RRM could be used for selection on level and persistency of litter size in pigs.

REFERENCES

Huisman, A.E. (2002). Genetic analysis of growth and feed intake patterns in pigs. Ph.D. Thesis, Wageningen Institute of Animal Sciences, The Netherlands.

Kovač, M., Groeneveld, E. (2002). VCE-5 User's Guide and Reference Manual Version 5.1. Institute of Animal Science and Animal Husbandry, FAL, D-31535 Neustadt, Germany.

Luković, Z., Gorjanc, G., Malovrh, Š., Kovač, M. (2003). Estimation of genetic parameters for number of piglets born alive using random regression model. 3rd Congress of the Genetic Society of Slovenia, Bled, May 31 – June 4, pp 243-245.

Meyer, K. (1998). Modeling 'repeated' records: covariance functions and random regression models to analyse animal breeding data. In: Proc. 6th WCGALP 25:517-520, Armidale, Australia.

Rothschild, M.F. & Bidanel, J.P.(1998). Biology and genetics of reproduction. In: The genetics of the pig (ed. Rothschild, M.F. & Ruvinsky, A.). Oxon, CAB International, pp 313-343.

SAS Institute (2001). The SAS System for Windows, Release 8.02. Cary, NC.

Van der Werf, J.H.J, Goddard, M.E., Meyer, K. (1998). The use of covariance function and random regressions for genetic evaluation of milk production based on test day records. J. Dairy Sci. 81, 3300-3308.

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